



SEQUENCE LISTING

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<120> TAO PROTEIN KINASE POLYPEPTIDES AND METHODS OF USE
THEREFOR

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Pro Glu Ala Phe Ser His Ser Tyr Pro Gly Ala Ser Ser Trp Ser His	
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Asn Pro Thr Gly Gly Ser Gly Pro His Trp Gly His Pro Met Gly Gly	
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Thr Pro Gln Ala Trp Gly His Pro Met Gln Gly Gly Pro Gln Pro Trp	
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<213> Rattus norvegicus

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Asp Asn Leu Gln Tyr Arg Lys Met Lys Lys Leu Leu Phe Gln Glu Ala
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Tyr Lys Ala Leu Arg Asn His Leu Leu Glu Thr Thr Pro Lys Ser Glu
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His Lys Ala Val Leu Lys Arg Leu Lys Glu Glu Gln Thr Arg Lys Leu
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Thr Gln Ala Leu Arg Leu Asp Glu Ala Gln Glu Ala Glu Cys Gln Val
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agtcattctg ggaaatggaa tataaggcac tcattgcatt catgttgaaa aggggcggct 180
tccgttccgc caattcaata caagtgatgc caagtgaacca aatatcaact ttcccatcat 240
actgtccttc atccatagct aagatcacct ctggagccat ccagtaaggt gtgcccacga 300
aggagttggc cagg 314
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<210> 7

<211> 370

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1)..(370)

<223> N = a, c, g or t/u

<400> 7

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tgcttttcca ataggttctt tattctctcg ctgcgttctt tctgaagggc agccagctcc 120
tcttcaatct tctgctcaag gtgtgggtctg cgcagagaca ctctctgctc tagcttctgg 180
agctcacgtt catgttgtgc ctctgttngn atcttgattt ggntctggta ggcgttgagc 240
agctccattt cctgctggag ctgtagcctc aaggcctggc attctgcttc ttgagcctca 300
tctagccgta acgcttgaga ggccatcatt tcatttatac tctgttcata ctgctctgcc 360
aaaatggcaa 370
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<210> 8

<211> 190

<212> DNA
<213> Homo sapiens

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caacagcaga aaaacttaaa ggccatggaa atgcaaatta aaaaacagtt tcaggacact 60
tgcaaagtac agaccaaaca gtataaagca ctcaagaatc accagttgga agttactcca 120
aagaatgagc acaaaacaat cttaaagaca ctgaaagatg agcagacaag aaaacttgcc 180
atdddggcag 190

<210> 9
<211> 61
<212> DNA
<213> Homo sapiens

<400> 9
gacgcagtat gaacagagta taaatgaaat gatggcctct caagcggtac ggctagatga 60
g 61

<210> 10
<211> 219
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1)..(219)
<223> N = a, c, g or t/u

<400> 10
acgagtcgcc cccagagagcta gaggacagga agctgcacac gttacagaag ctacgcattg 60
atctgatccg ttacagcac cagacggaac tggaaaacca gctggagtag aataagagga 120
gagaaagaga actgcacaga aagcatgtca tggaaacttcg gcaacagcca aaaaacttaa 180
aggccatgga antgcaattt aaaaacagc tccaggaaa 219

<210> 11
<211> 85
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1)..(85)
<223> N = a, c, g or t/u

<400> 11

gtgcatatgg tatatttnat tcatttttgt aaagcgttct gttttgtgtt tactaattgg 60
gatgtcatag tacttggtcg ccggg 85

<210> 12
<211> 46
<212> DNA
<213> Homo sapiens

<400> 12
ctcacttggg tactacagtg tggaagctga gtgcatatgg tatatt 46

<210> 13
<211> 116
<212> DNA
<213> Homo sapiens

<400> 13
gatatttggg cattgggtat cacgtgtata gagctggccg aacgtcgtcc accattgttc 60
agtatgaatg caatgtctgc cctctaccat attgctcaaa atgacctcc aactct 116

<210> 14
<211> 118
<212> DNA
<213> Homo sapiens

<400> 14
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aacgtgctgc tctcggagca gggatgatgtg aagatggcag acttcggtgt ggctggca 118

<210> 15
<211> 110
<212> DNA
<213> Homo sapiens

<400> 15
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tacaagggga tcgacaacca caccaaggaa gtggtggcca tcaagatcat 110

<210> 16
<211> 134
<212> DNA
<213> Homo sapiens

<400> 16

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ttttcattaa ggtaagggggg ttcaccttcc accatttcaa ttgccataat tccaagagac 120
cagatatcaa cttt 134

<210> 17

<211> 278

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 17

Met Ala Pro Ala Val Leu Gln Lys Pro Gly Val Ile Lys Asp Pro Ser
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20 25 30

Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Tyr Asp Lys Lys
35 40 45

Asn Glu Gln Thr Val Ala Ile Lys Lys Met Asn Phe Ser Gly Lys Gln
50 55 60

Ala Val Glu Lys Trp Asn Asp Ile Leu Lys Glu Val Ser Phe Leu Asn
65 70 75 80

Thr Val Val His Pro His Ile Val Asp Tyr Lys Ala Cys Phe Leu Lys
85 90 95

Asp Thr Thr Cys Trp Leu Val Met Glu Tyr Cys Ile Gly Ser Ala Ala
100 105 110

Asp Ile Val Asp Val Leu Arg Lys Gly Met Arg Glu Val Glu Ile Ala
115 120 125

Ala Ile Cys Ser Gln Thr Leu Asp Ala Leu Arg Tyr Leu His Ser Leu
130 135 140

Lys Arg Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Ser Asp
145 150 155 160

His Ala Ile Val Lys Leu Ala Asp Phe Gly Ser Ala Ser Leu Val Asp
165 170 175

Pro Ala Gln Thr Phe Ile Gly Thr Pro Phe Phe Met Ala Pro Glu Val
180 185 190

Ile Leu Ala Met Asp Glu Gly His Tyr Thr Asp Arg Ala Asp Ile Trp
 195 200 205

Ser Leu Gly Ile Thr Cys Ile Glu Leu Ala Glu Arg Arg Pro Pro Leu
 210 215 220

Phe Ser Met Asn Ala Met Ser Ala Leu Tyr His Ile Ala Gln Asn Asp
 225 230 235 240

Pro Pro Thr Leu Ser Pro Ile Asp Thr Ser Glu Gln Pro Glu Trp Ser
 245 250 255

Leu Glu Phe Val Gln Phe Ile Asp Lys Cys Leu Arg Lys Pro Ala Glu
 260 265 270

Glu Arg Met Ser Ala Glu
 275

<210> 18
 <211> 273
 <212> PRT
 <213> C. ELEGANS

<400> 18
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Glu Ile Cys Ser Asp Gly Asp Pro Ser Thr Lys Tyr Ala Asn Leu Val
 20 25 30

Lys Ile Gly Gln Gly Ala Ser Gly Gly Val Tyr Thr Ala Tyr Glu Ile
 35 40 45

Gly Thr Asn Val Ser Val Ala Ile Lys Gln Met Asn Leu Glu Lys Gln
 50 55 60

Pro Lys Lys Glu Leu Ile Ile Asn Glu Ile Leu Val Met Lys Gly Ser
 65 70 75 80

Lys His Pro Asn Ile Val Asn Phe Ile Asp Ser Tyr Val Leu Lys Gly
 85 90 95

Asp Leu Trp Val Ile Met Glu Tyr Met Glu Gly Gly Ser Leu Thr Val
 100 105 110

Asp Val Val Thr His Cys Ile Leu Thr Glu Gly Gln Ile Gly Ala Val
 115 120 125

Cys Arg Glu Thr Leu Ser Gly Leu Glu Phe Leu His Ser Lys Gly Val
 130 135 140

Leu His Arg Asp Ile Lys Ser Asp Asn Ile Leu Leu Ser Met Glu Gly
 145 150 155 160

Asp Ile Lys Leu Thr Asp Phe Gly Phe Cys Ala Gln Ile Asn Glu Leu
 165 170 175

Asn Leu Lys Arg Thr Thr Met Val Gly Thr Pro Tyr Trp Met Ala Pro
 180 185 190

Glu Val Val Ser Arg Lys Glu Tyr Gly Pro Lys Val Asp Ile Trp Ser
 195 200 205

Leu Gly Ile Met Ile Ile Glu Met Ile Glu Gly Glu Pro Pro Tyr Leu
 210 215 220

Asn Glu Thr Pro Leu Arg Ala Leu Tyr Leu Ile Ala Thr Asn Gly Thr
 225 230 235 240

Pro Lys Leu Lys Glu Pro Glu Asn Leu Ser Ser Ser Leu Lys Lys Phe
 245 250 255

Leu Asp Trp Cys Leu Cys Cys Val Glu Pro Glu Asp Arg Ala Ser Ala
 260 265 270

Thr

<210> 19

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 Primer

<220>

<221> modified_base

<222> (1)..(33)

<223> N = a, c g, or t/u

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<211> 21
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<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<220>
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<222> (1)..(21)
<223> N = inosineI

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21

<210> 21
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<220>
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<222> (1)..(28)
<223> N = inosineI

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28

<210> 22
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
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Primer

<220>

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<222> (1)..(30)

<223> N = inosineI

<400> 22

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30

<210> 23

<211> 20

<212> PRT

<213> Rattus norvegicus

<400> 23

Thr Lys Asp Ala Val Arg Glu Leu Asp Asn Leu Gln Tyr Arg Lys Met

1

5

10

15

Lys Lys Leu Leu

20

<210> 24

<211> 19

<212> PRT

<213> Rattus norvegicus

<400> 24

Lys Lys Glu Leu Asn Ser Phe Leu Glu Ser Gln Lys Arg Glu Tyr Lys

1

5

10

15

Leu Arg Lys

<210> 25

<211> 20

<212> PRT

<213> Rattus norvegicus

<400> 25

Arg Glu Leu Arg Glu Leu Glu Gln Arg Val Ser Leu Arg Arg Ala Leu

1

5

10

15

Leu Glu Gln Lys

20

<210> 26

<211> 8
<212> PRT
<213> Rattus norvegicus

<400> 26
His Arg Asp Ile Lys Ala Gly Asn
1 5

<210> 27
<211> 3781
<212> DNA
<213> C. ELEGANS

<220>
<221> CDS
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ttactcatcc atcaacaaca aaatcaaaca agacaagaaa aacatcagaa aatttcaaaa 180

attaataaca atacacattt attaataatc aaaaattcat tttcgttggc gccgcgcttc 240

tcgaatatac ggagaacgga ggaggtggtg gagttacg atg gcg cct gcc gtc tta 296
Met Ala Pro Ala Val Leu
1 5

caa aaa ccc ggt gtt atc aag gat cca tcg att gct gca ttg ttc agt 344
Gln Lys Pro Gly Val Ile Lys Asp Pro Ser Ile Ala Ala Leu Phe Ser
10 15 20

aat aag gat cca gag cag aga tat caa gat tta aga gaa att gga cat 392
Asn Lys Asp Pro Glu Gln Arg Tyr Gln Asp Leu Arg Glu Ile Gly His
25 30 35

gga tct ttt gga gct gtc tat ttt gca tat gac aaa aaa aat gag cag 440
Gly Ser Phe Gly Ala Val Tyr Phe Ala Tyr Asp Lys Lys Asn Glu Gln
40 45 50

act gtt gcg att aaa aag atg aat ttt agt gga aaa cag gct gtc gaa 488
Thr Val Ala Ile Lys Lys Met Asn Phe Ser Gly Lys Gln Ala Val Glu
55 60 65 70

aaa tgg aat gat att ctt aaa gaa gtg tct ttt ctg aat aca gtt gtt 536

Lys Trp Asn Asp Ile Leu Lys Glu Val Ser Phe Leu Asn Thr Val Val	
75 80 85	
cat cca cat att gtc gac tac aag gct tgt ttt ctt aag gac act aca	584
His Pro His Ile Val Asp Tyr Lys Ala Cys Phe Leu Lys Asp Thr Thr	
90 95 100	
tgt tgg ctt gtg atg gag tac tgt att ggc tct gca gcc gat ata gtg	632
Cys Trp Leu Val Met Glu Tyr Cys Ile Gly Ser Ala Ala Asp Ile Val	
105 110 115	
gat gtc ttg cga aaa gga atg cga gaa gtc gaa atc gct gcg att tgc	680
Asp Val Leu Arg Lys Gly Met Arg Glu Val Glu Ile Ala Ala Ile Cys	
120 125 130	
tct caa act ttg gat gct ctt cga tat ctt cac tct ctg aag cga ata	728
Ser Gln Thr Leu Asp Ala Leu Arg Tyr Leu His Ser Leu Lys Arg Ile	
135 140 145 150	
cat cga gat att aaa gct gga aat att ctg cta tct gat cat gct att	776
His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Ser Asp His Ala Ile	
155 160 165	
gtt aaa cta gct gat ttc gga tcc gca tcc ctg gta gat ccg gct caa	824
Val Lys Leu Ala Asp Phe Gly Ser Ala Ser Leu Val Asp Pro Ala Gln	
170 175 180	
act ttc atc gga acg ccg ttt ttc atg gcc cca gag gta att ctg gca	872
Thr Phe Ile Gly Thr Pro Phe Phe Met Ala Pro Glu Val Ile Leu Ala	
185 190 195	
atg gat gag ggt cac tac acg gat cgt gca gat att tgg tca ttg ggt	920
Met Asp Glu Gly His Tyr Thr Asp Arg Ala Asp Ile Trp Ser Leu Gly	
200 205 210	
atc acg tgt ata gag ctg gcc gaa cgt cgt cca cca ttg ttc agt atg	968
Ile Thr Cys Ile Glu Leu Ala Glu Arg Arg Pro Pro Leu Phe Ser Met	
215 220 225 230	
aat gca atg tct gcc ctc tac cat att gct caa aat gat cct cca act	1016
Asn Ala Met Ser Ala Leu Tyr His Ile Ala Gln Asn Asp Pro Pro Thr	
235 240 245	
ctt tct cca att gac act agc gaa caa ccg gaa tgg tcg ctg gaa ttc	1064
Leu Ser Pro Ile Asp Thr Ser Glu Gln Pro Glu Trp Ser Leu Glu Phe	
250 255 260	
gtt caa ttt ata gac aaa tgt ctt cga aaa cca gca gaa gag cga atg	1112

Val	Gln	Phe	Ile	Asp	Lys	Cys	Leu	Arg	Lys	Pro	Ala	Glu	Glu	Arg	Met	
	265						270					275				
tca	gct	gaa	gaa	tgc	ttt	cga	cat	cca	ttc	att	caa	cgg	tct	cgc	cca	1160
Ser	Ala	Glu	Glu	Cys	Phe	Arg	His	Pro	Phe	Ile	Gln	Arg	Ser	Arg	Pro	
	280					285					290					
tca	gac	aca	att	cag	gaa	ctc	att	cag	aga	acg	aaa	aat	atg	gta	tta	1208
Ser	Asp	Thr	Ile	Gln	Glu	Leu	Ile	Gln	Arg	Thr	Lys	Asn	Met	Val	Leu	
	295				300				305						310	
gag	ttg	gat	aat	ttt	caa	tac	aaa	aag	atg	aga	aaa	ctc	atg	tat	ttg	1256
Glu	Leu	Asp	Asn	Phe	Gln	Tyr	Lys	Lys	Met	Arg	Lys	Leu	Met	Tyr	Leu	
			315					320					325			
gat	gaa	aca	gaa	gga	aaa	gaa	gga	agt	gaa	gga	aat	gga	gca	tct	gat	1304
Asp	Glu	Thr	Glu	Gly	Lys	Glu	Gly	Ser	Glu	Gly	Asn	Gly	Ala	Ser	Asp	
		330					335					340				
gat	tta	gat	ttt	cat	gga	aat	gaa	gct	aat	tca	att	gga	aga	gca	gga	1352
Asp	Leu	Asp	Phe	His	Gly	Asn	Glu	Ala	Asn	Ser	Ile	Gly	Arg	Ala	Gly	
	345					350				355						
gat	tct	gcg	tca	tct	cga	agt	gct	tct	ctt	act	tct	ttc	cga	tca	atg	1400
Asp	Ser	Ala	Ser	Ser	Arg	Ser	Ala	Ser	Leu	Thr	Ser	Phe	Arg	Ser	Met	
	360				365				370							
cag	agt	agt	gga	gga	gct	ggt	ctt	tta	gtg	tcc	acc	aat	acg	acg	ggt	1448
Gln	Ser	Ser	Gly	Gly	Ala	Gly	Leu	Leu	Val	Ser	Thr	Asn	Thr	Thr	Gly	
	375			380				385					390			
gct	atg	gat	aat	gtg	cat	gga	tcc	tct	gga	tac	ggt	aat	gga	agt	agt	1496
Ala	Met	Asp	Asn	Val	His	Gly	Ser	Ser	Gly	Tyr	Gly	Asn	Gly	Ser	Ser	
			395			400			405							
tcg	acg	acg	agc	tcc	gca	cgc	cgc	cgt	cct	cca	att	cct	tcg	caa	atg	1544
Ser	Thr	Thr	Ser	Ser	Ala	Arg	Arg	Arg	Pro	Pro	Ile	Pro	Ser	Gln	Met	
			410				415					420				
ctc	tct	tct	aca	tca	acg	tct	ggt	gtt	gga	act	atg	ccg	agt	cat	gga	1592
Leu	Ser	Ser	Thr	Ser	Thr	Ser	Gly	Val	Gly	Thr	Met	Pro	Ser	His	Gly	
	425					430			435							
tca	gtt	gga	gca	tcg	att	acg	gcg	atc	gca	gtc	aat	cca	aca	ccg	tct	1640
Ser	Val	Gly	Ala	Ser	Ile	Thr	Ala	Ile	Ala	Val	Asn	Pro	Thr	Pro	Ser	
	440					445			450							
cct	tca	gaa	cct	atc	cca	aca	tca	caa	cca	aca	tcg	aaa	tca	gaa	tca	1688

Pro Ser Glu Pro Ile Pro Thr Ser Gln Pro Thr Ser Lys Ser Glu Ser	
455 460 465 470	
tct tct ata ctc gaa act gca cac gat gat cct ttg gac acg tcg ata	1736
Ser Ser Ile Leu Glu Thr Ala His Asp Asp Pro Leu Asp Thr Ser Ile	
475 480 485	
cgt gct cca gtg aaa gac ttg cat atg ccg cat cga gca gtc aag gaa	1784
Arg Ala Pro Val Lys Asp Leu His Met Pro His Arg Ala Val Lys Glu	
490 495 500	
cga ata gcc acg ttg caa aat cac aaa ttc gcg acg ctt cgt tcc cag	1832
Arg Ile Ala Thr Leu Gln Asn His Lys Phe Ala Thr Leu Arg Ser Gln	
505 510 515	
aga ata atc aat cag gaa caa gaa gaa tat acg aaa gag aac aat atg	1880
Arg Ile Ile Asn Gln Glu Gln Glu Glu Tyr Thr Lys Glu Asn Asn Met	
520 525 530	
tat gag caa atg agc aag tac aag cat cta cga caa gca cat cac aaa	1928
Tyr Glu Gln Met Ser Lys Tyr Lys His Leu Arg Gln Ala His His Lys	
535 540 545 550	
gag ctc caa caa ttt gaa gaa cga tgt gca tta gat aga gag caa ctg	1976
Glu Leu Gln Gln Phe Glu Glu Arg Cys Ala Leu Asp Arg Glu Gln Leu	
555 560 565	
cgt gtg aaa atg gat cga gaa ctc gaa caa ttg aca acg aca tac tcg	2024
Arg Val Lys Met Asp Arg Glu Leu Glu Gln Leu Thr Thr Thr Tyr Ser	
570 575 580	
aaa gaa aag atg aga gtg agg tgt tca cag aat aat gaa cta gac aaa	2072
Lys Glu Lys Met Arg Val Arg Cys Ser Gln Asn Asn Glu Leu Asp Lys	
585 590 595	
cgg aaa aaa gat atc gaa gat ggg gag aaa aag atg aaa aag acg aaa	2120
Arg Lys Lys Asp Ile Glu Asp Gly Glu Lys Lys Met Lys Lys Thr Lys	
600 605 610	
aat agt caa aat cag cag cag atg aaa ctg tat tca gcg caa caa ttg	2168
Asn Ser Gln Asn Gln Gln Gln Met Lys Leu Tyr Ser Ala Gln Gln Leu	
615 620 625 630	
aaa gaa tac aag tat aac aag gag gca cag aaa aca cga tta cga agt	2216
Lys Glu Tyr Lys Tyr Asn Lys Glu Ala Gln Lys Thr Arg Leu Arg Ser	
635 640 645	
ctg aac atg cct cga agt act tat gag aac gca atg aaa gaa gtg aaa	2264

Leu Asn Met Pro Arg Ser Thr Tyr Glu Asn Ala Met Lys Glu Val Lys	
650 655 660	
gcc gat ctg aat cga gtg aaa gat gca cgg gaa aat gat ttt gac gag	2312
Ala Asp Leu Asn Arg Val Lys Asp Ala Arg Glu Asn Asp Phe Asp Glu	
665 670 675	
aag ctt cgt gca gaa ctt gaa gat gaa att gta agg tat cgc agg caa	2360
Lys Leu Arg Ala Glu Leu Glu Asp Glu Ile Val Arg Tyr Arg Arg Gln	
680 685 690	
caa ctc agt aat ctt cat caa ttg gaa gaa caa ttg gat gat gaa gac	2408
Gln Leu Ser Asn Leu His Gln Leu Glu Glu Gln Leu Asp Asp Glu Asp	
695 700 705 710	
gta aac gtg caa gaa cgc caa atg gac acg cgt cac gga tta ctg tca	2456
Val Asn Val Gln Glu Arg Gln Met Asp Thr Arg His Gly Leu Leu Ser	
715 720 725	
aag cag cat gaa atg acg cgc gat ttg gaa ata cag cat ctc aac gag	2504
Lys Gln His Glu Met Thr Arg Asp Leu Glu Ile Gln His Leu Asn Glu	
730 735 740	
ctt cac gcg atg aaa aaa cga cat ttg gag aca caa cac gag gcg gaa	2552
Leu His Ala Met Lys Lys Arg His Leu Glu Thr Gln His Glu Ala Glu	
745 750 755	
tcg gca agt caa aat gag tac aca cag agg caa cag gat gaa ttg aga	2600
Ser Ala Ser Gln Asn Glu Tyr Thr Gln Arg Gln Gln Asp Glu Leu Arg	
760 765 770	
aaa aag cat gcg atg cag tca aga caa cag cca aga gat tta aag atc	2648
Lys Lys His Ala Met Gln Ser Arg Gln Gln Pro Arg Asp Leu Lys Ile	
775 780 785 790	
caa gaa gca caa att cga aaa caa tac cga caa gtt gtg aag act cag	2696
Gln Glu Ala Gln Ile Arg Lys Gln Tyr Arg Gln Val Val Lys Thr Gln	
795 800 805	
act cgc caa ttt aag ctc tac ctt aca caa atg gtg caa gta gtt cca	2744
Thr Arg Gln Phe Lys Leu Tyr Leu Thr Gln Met Val Gln Val Val Pro	
810 815 820	
aaa gat gaa caa aaa gag ctc acg tct cga cta aaa cag gat caa atg	2792
Lys Asp Glu Gln Lys Glu Leu Thr Ser Arg Leu Lys Gln Asp Gln Met	
825 830 835	
caa aaa gtc gca ctt ctt gct tca caa tac gaa agt caa atc aaa aaa	2840

Gln	Lys	Val	Ala	Leu	Leu	Ala	Ser	Gln	Tyr	Glu	Ser	Gln	Ile	Lys	Lys		
840						845					850						
atg gtt cag gat aag aca gtg aag ctc gag tcg tgg caa gaa gat gaa	2888																
Met Val Gln Asp Lys Thr Val Lys Leu Glu Ser Trp Gln Glu Asp Glu																	
855	860	865	870														
caa cgg gtt ctt agt gag aag ttg gag aaa gaa ttg gaa gaa ttg att	2936																
Gln Arg Val Leu Ser Glu Lys Leu Glu Lys Glu Leu Glu Glu Leu Ile																	
875	880	885															
gct tat cag aag aag acg aga gcc aca tta gaa gag cag att aaa aag	2984																
Ala Tyr Gln Lys Lys Thr Arg Ala Thr Leu Glu Glu Gln Ile Lys Lys																	
890	895	900															
gaa cgt acg gca ctc gaa gaa cga att ggc aca cga cgt gca atg ctt	3032																
Glu Arg Thr Ala Leu Glu Glu Arg Ile Gly Thr Arg Arg Ala Met Leu																	
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gaa cag aag att att gaa gaa cgc gaa caa atg gga gaa atg cgt cga	3080																
Glu Gln Lys Ile Ile Glu Glu Arg Glu Gln Met Gly Glu Met Arg Arg																	
920	925	930															
cta aag aag gag caa atc cgt gat cga cac agt caa gaa cgc cat cgt	3128																
Leu Lys Lys Glu Gln Ile Arg Asp Arg His Ser Gln Glu Arg His Arg																	
935	940	945	950														
ctc gag aat cat ttc gta cgg acg ggc tcg acg agc aga agt tct ggt	3176																
Leu Glu Asn His Phe Val Arg Thr Gly Ser Thr Ser Arg Ser Ser Gly																	
955	960	965															
ggg atc gct cct ggt gtt ggg aat tca agc agt att cag atg gct atg	3224																
Gly Ile Ala Pro Gly Val Gly Asn Ser Ser Ser Ile Gln Met Ala Met																	
970	975	980															
tag aatgatgttg tctctttaatt ctactacact tcgggtcgtc taccaattgt	3277																
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 35 40 45
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 Glu Ile Ala Ala Ile Cys Ser Gln Thr Leu Asp Ala Leu Arg Tyr Leu
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 His Ser Leu Lys Arg Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu
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 Pro Glu Val Ile Leu Ala Met Asp Glu Gly His Tyr Thr Asp Arg Ala
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Lys	Met	Lys	Lys	Thr	Lys	Asn	Ser	Gln	Asn	Gln	Gln	Gln	Met	Lys	Leu
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